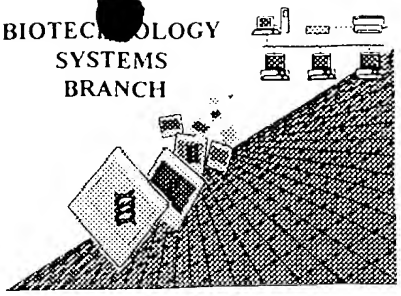
0460

BIOTECHNOLOGY SYSTEMS BRANCH



RAW SEQUENCE LISTING ERROR REPORT

The Biotechnology Systems Branch of the Scientific and Technical Information Center (STIC) detected errors when processing the following computer readable form:

Application Serial Number: 09/759,281

Source: OIPE

Date Processed by STIC: 1-29-01

THE ATTACHED PRINTOUT EXPLAINS DETECTED ERRORS.
PLEASE FORWARD THIS INFORMATION TO THE APPLICANT BY EITHER:

1) **INCLUDING A COPY OF THIS PRINTOUT IN YOUR NEXT COMMUNICATION TO THE APPLICANT, WITH A NOTICE TO COMPLY or,**
2) **TELEPHONING APPLICANT AND FAXING A COPY OF THIS PRINTOUT, WITH A NOTICE TO COMPLY**

FOR CRF SUBMISSION QUESTIONS, PLEASE CONTACT MARK SPENCER, 703-308-4212.

FOR SEQUENCE RULES INTERPRETATION, PLEASE CONTACT ROBERT WAX, 703-308-4216.
PATENTIN 2.1 e-mail help: patin21help@uspto.gov or phone 703-306-4119 (R. Wax)
PATENTIN 3.0 e-mail help: patin3help@uspto.gov or phone 703-306-4119 (R. Wax)

TO REDUCE ERRORED SEQUENCE LISTINGS, PLEASE USE THE **CHECKER VERSION 3.0 PROGRAM**, ACCESSIBLE THROUGH THE U.S. PATENT AND TRADEMARK OFFICE WEBSITE. SEE BELOW:

Checker Version 3.0

The Checker Version 3.0 application is a state-of the-art Windows based software program employing a logical and intuitive user-interface to check whether a sequence listing is in compliance with format and content rules. Checker Version 3.0 works for sequence listings generated for the original version of 37 CFR §§1.821 – 1.825 effective October 1, 1990 (old rules) and the revised version (new rules) effective July 1, 1998 as well as World Intellectual Property Organization (WIPO) Standard ST.25.
Checker Version 3.0 replaces the previous DOS-based version of Checker, and is Y2K-compliant. Checker allows public users to check sequence listings in Computer Readable form (CRF) before submitting them to the United States Patent and Trademark Office (USPTO). Use of Checker prior to filing the sequence listing is expected to result in fewer errored sequence listings, thus saving time and money.

Checker Version 3.0 can be down loaded from the USPTO website at the following address:
http://www.uspto.gov/web/offices/pac/checker

New Sequence Listing Error Summary

ERROR DETECTED **SUGGESTED CORRECTION** SERIAL NUMBER: 09/759,281

ATTN: NEW RULES CASES: PLEASE DISREGARD ENGLISH "ALPHA" HEADERS, WHICH WERE INSERTED BY PTO SOFTWARE

1 ____	Wrapped Nucleics	The number/text at the end of each line "wrapped" down to the next line. This may occur if your file was retrieved in a word processor after creating it. Please adjust your right margin to .3, as this will prevent "wrapping".
2 ____	Wrapped Aminos	The amino acid number/text at the end of each line "wrapped " down to the next line. This may occur if your file was retrieved in a word processor after creating it. Please adjust your right margin to .3, as this will prevent "wrapping".
3 ____	Incorrect Line Length	The rules require that a line not exceed 72 characters in length. This includes spaces.
4 ____	Misaligned Amino Acid Numbering	The numbering under each 5th amino acid is misaligned. This may be caused by the use of tabs between the numbering. It is recommended to delete any tabs and use spacing between the numbers.
5 ✓	Non-ASCII	This file was not saved in ASCII (DOS) text, as required by the Sequence Rules. Please ensure your subsequent submission is saved in ASCII text so that it can be processed.
6 ____	Variable Length	Sequence(s) ____ contain n's or Xaa's which represented more than one residue. As per the rules, each n or Xaa can only represent a single residue. Please present the maximum number of each residue having variable length and indicate in the (ix) feature section that some may be missing.
7 ____	PatentIn ver. 2.0 "bug"	A "bug" in PatentIn version 2.0 has caused the <220>-<223> section to be missing from amino acid sequence(s) _____. Normally, PatentIn would automatically generate this section from the previously coded nucleic acid sequence. Please manually copy the relevant <220>-<223> section to the subsequent amino acid sequence. **This applies primarily to the mandatory <220>-<223> sections for Artificial or Unknown sequences.**
8 ____	Skipped Sequences (OLD RULES)	Sequence(s) ____ missing. If intentional, please use the following format for each skipped sequence: **(2) INFORMATION FOR SEQ ID NO:X:** **(i) SEQUENCE CHARACTERISTICS:**(Do not insert any headings under "SEQUENCE CHARACTERISTICS") **(xi) SEQUENCE DESCRIPTION:SEQ ID NO:X:** **This sequence is intentionally skipped** Please also adjust the "(iii) NUMBER OF SEQUENCES:" response to include the skipped sequence(s).
9 ____	Skipped Sequences (NEW RULES)	Sequence(s) ____ missing. If intentional, please use the following format for each skipped sequence. **<210> sequence id number** **<400> sequence id number** **000**
10 ____	Use of n's or Xaa's (NEW RULES)	Use of n's and/or Xaa's have been detected in the Sequence Listing. Use of <220> to <223> is MANDATORY if n's or Xaa's are present. In <220> to <223> section, please explain location of **n** or **Xaa**, and which residue **n** or **Xaa** represents.
11 ____	Use of <213>Organism (NEW RULES)	Sequence(s) _____ are missing this mandatory field or its response.
12 ____	Use of <220>Feature (NEW RULES)	Sequence(s) ____ are missing the <220>Feature and associated headings. Use of <220> to <223> is MANDATORY if <213>ORGANISM is "Artificial" or "Unknown" **Please explain source of genetic material in <220> to <223> section.** (See "Federal Register," 6/01/98, Vol. 63, No. 104, pp. 29631-32) (Sec. 1.823 of new Rules)
13 ____	PatentIn ver. 2.0 "bug"	**Please do not use "Copy to Disk" function of PatentIn version 2.0.** This causes a corrupted file, resulting in missing mandatory numeric identifiers and responses (as indicated on raw sequence listing). Instead, please use "File Manager" or any other means to copy file to floppy disk.

Does Not Comply
Corrected Diskette Needed

SEQUENCE LISTING

GENERAL INFORMATION:

(i) ← Move to same line

APPLICANT: PEREGRINO FERREIRA, Paulo;

GESSIEN KROON, Erna;

PIMENTA DOS REIS, Karlisson Jennner;

BIAS FORTES FERRAZ, Isabella;

CERQUEIRA LEITE, Romulo.

* File not saved in ASCII text See #5 on the Error Summary Sheet.

(ii) ← Same line

TITLE OF INVENTION: Method and composition for the diagnosis of equine infectious anemia virus disease by using the recombinant capsid protein virus (p26)

Delete numerals in the margin

(iii) ← Same line

NUMBER OF SEQUENCES: 1

(iv) ←

CORRESPONDENCE ADDRESS:

(A) ←

ADDRESSEE: Universidade Federal de Minas Gerais - CTIT

(B) ←

STREET: Avenida Antônio Carlos, 6627 Bairro São Francisco

(C) ←

CITY: Belo Horizonte

(D) ←

STATE: Minas Gerais

(E) ←

COUNTRY: BRAZIL

(F) ←

ZIP: 31270-901

(v) ←

COMPUTER READABLE FORM:

(A)

Move all response to where arrows indicate.

Example →

(i) GENERAL INFORMATION:
(i) APPLICANT:
(ii) TITLE OF INVENTION:
(iii) NUMBER OF SEQUENCES:
(iv) CORRESPONDENCE ADDRESS:
(A) ADDRESSEE:
(B) STREET:
(C) CITY:
(D) STATE:
(E) COUNTRY:
(F) ZIP:

(A) ←

MEDIUM TYPE: diskette – 3.50 inch, 1.44 Mb storage

(B) ←

COMPUTER: IBM compatible

(C) ←

OPERATING SYSTEM: Windows 98

(D) ←

SOFTWARE: Office premium

(vi) ←

CURRENT APPLICATION DATA:

(A) ← 09/759,281

APPLICATION NUMBER: U.S. ~~09/331,262~~

(B) ←

FILING DATE:

(C) ←

CLASSIFICATION: C12Q1/70

(vii) ←

PRIOR APPLICATION DATA

(A) ←

APPLICATION NUMBER: PI 9606273-8

(B) ←

FILING DATE: 18-DEC-1996

(2) ←

INFORMATION FOR SEQ ID N0:1:

(i) ←

SEQUENCE CHARACTERISTICS:

(A) ←

LENGHT: 252 amino acids → There are 321 amino acids shown see p 5

(B) ←

TYPE: amino acid

(D) ←

TOPOLOGY: linear

Delete the numerals in the margin

Move all response to where arrows indicate.

(V) COMPUTER READABLE FORM:
(A) MEDIUM TYPE:
(B) COMPUTER:
(C) OPERATING SYSTEM:
(D) SOFTWARE:
(VI) CURRENT APPLICATION DATA:
(A) APPLICATION NUMBER:
(B) FILING DATE:
(C) CLASSIFICATION:
(VII) PRIOR APPLICATION DATA
(A) APPLICATION NUMBER:
(B) FILING DATE:
(VIII) ATTORNEY/AGENT INFORMATION:
(A) NAME:
(B) REGISTRATION NUMBER:
(C) REFERENCE/DOCKET NUMBER:
(IX) TELECOMMUNICATION INFORMATION:
(A) TELEPHONE:
(B) TELEFAX:
(C) TELEX:

(ii)
MOLECULE TYPE : protein

(vi)
ORIGINAL SOURCE

(A)
ORGANISM : equine infectious anemia virus

(ix)
FEATURE:

(A)
NAME: p26

(x)
PUBLICATION INFORMATION

(A)
AUTHORS:

(B)
TITLE: (

C)
JOURNAL:

(D)
VOLUME:

(F)
PAGES:

(G)
DATE:

(xi)
SEQUENCE DESCRIPTION: SEQ ID NO:1

His His His His His His Gly Ser Pro Gly Asn Pro Leu Thr Trp

5 10 15

move responses to where arrows indicate.

(2) INFORMATION FOR SEQ ID NO: X:
(i) SEQUENCE CHARACTERISTICS:
(A) LENGTH:
(B) TYPE:
(C) STRANDEDNESS:
(D) TOPOLOGY:
(ii) MOLECULE TYPE:
(iii) HYPOTHETICAL:
(iv) ANTI-SENSE:
(v) FRAGMENT TYPE:
(vi) ORIGINAL SOURCE:
(A) ORGANISM:

Delete numerals in the margin.

Do not include headings which have no response.

Ser Lys Ala Leu Lys Lys Leu Glu Lys Val Thr Val Gln Gly Ser
20 25 30
Gln Lys Leu Thr Thr Gly Asn Cys Na Trp Ala Leu Ser Leu Val
35 40 45
Asp Leu Phe His Asp Thr Asn Phe Val Lys Glu Lys Asp Trp Gln
50 55 60
Leu Arg Asp Val Ile Pro Leu Leu Glu Asp Val Thr Gln Thr Val
65 70 75
Ser Gly Gln Glu Arg Glu Ala Phe Glu Arg Thr Trp Trp Ala Ile
80 85 90
Ser Ala Val Lys Met Gly Leu Gln Ile Asn AsnVal Val Asp Gly
95 100 105
Lys Ala Ser Phe Gln Leu Leu Arg Ala Lys Tyr Glu Lys Lys Thr
110 115 120
Ala Asn Lys Lys Gln Ser Glu Pro Ser Glu Glu Tyr Pro Ile Met
125 130 135
Ile Asp Gly Ala Gly Asn Arg Asn Phe Arg Pro Leu Thr Pro Arg
140 145 150
Gly Tyr Thr Thr Trp Val AsnThr Ile Gln Thr Asn Gly Leu Leu
155 160 165
Asn Glu Ala Ser Gln Asn Leu Phe Gly Ile Leu Ser Val Asp Cys
170 175 180
Thr Ser Glu Glu Met Asn Ala Phe Leu Asp Val Val Pro Gly Gln
185 190 195
Ala Gly Gln Lys Gln Ile Leu Leu Asp Ala Ile Asp Lys Ile Ala
200 205 210
Asp Asp Trp Asp Asn Arg His Pro Leu Pro Asn Ala Pro Leu Val
215 220 225
Ala Pro Pro Gln Gly Pro Ile Pro Met Thr Ala Arg Phe Ile Arg
230 235 240
Gly Leu Gly Val Pro Arg Glu Arg Gln Met Glu Pro
245 250

Delete numerals in the margin

Asn Cys Val Val Gln Ser Phe Gly Val Ile Gly Gln Ala His Leu.
255? 260 265 270
Glu Leu Pro Arg Pro Asn Lys Arg Ile Arg Asn Gln. Ser Phe Asn
275 280 285
Gln Tyr Asn Cys Ser Ile Asn. Asn Lys Thr Glu Leu Glu Thr Trp
290 295 300
Lys Leu.Val Lys Thr Ser Gly Val Thr Pro Leu Pro. Ile Ser Ser
305 310 315
Glu Ala Asn Thr Gly Leu
320